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OM protein - protein search, using sw model

Run On: February 11, 2003, 19:44:29 ; Search time 28.6571 Seconds
(without alignments)
3178.015 Million cell updates/sec

Title: US-09-497-967-6
Perfect score: 2342
Sequence: 1 MKYNILLIILISIFINELRA.....STTFAKFLUSILLFISFYLL 442

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_invertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2342	100.0	442	5	Q9XZG2
2	2087	89.1	395	5	Q27208
3	1333	56.9	460	5	Q962N5
4	921	39.3	468	5	Q9BMH3
5	281.5	12.0	371	5	Q9GPP0
6	231	9.9	316	5	Q9GPP3
7	230	9.8	316	5	Q9GPP4
8	229	9.8	305	5	Q9GPP2
9	222	9.5	560	5	Q9U013
10	219.5	9.4	548	5	Q9GQ45
11	214.5	9.2	709	5	Q9XTJ7
12	212.5	9.1	704	5	Q9U048
13	212	9.1	1274	5	Q24977
14	210.5	9.0	557	5	Q24977
15	210.5	9.0	597	5	Q07317
16	210.5	9.0	1154	5	Q9GQ46

17	210.5	9.0	1274	5	Q9NGL3
18	206	8.8	594	5	Q24970
19	205.5	8.8	709	5	Q97444
20	205	8.8	1459	5	Q17084
21	199	8.5	397	5	Q95V71
22	198.5	8.5	423	5	Q9U697
23	196.5	8.4	719	5	Q9U021
24	195.5	8.3	1372	5	P91526
25	194.5	8.3	350	5	Q94589
26	194.5	8.3	667	5	Q9XTK3
27	194.5	8.3	719	5	Q9U019
28	194.5	8.3	1168	5	Q9U7S8
29	191.5	8.2	436	5	Q27197
30	191.5	8.2	1551	5	Q9NGV4
31	191.5	8.2	3396	5	Q9VM55
32	190	8.1	5374	11	Q99ND0
33	189	8.1	645	5	Q97448
34	187.5	8.0	421	5	Q95V69
35	186.5	8.0	504	5	Q95V69
36	184	7.9	394	5	Q9GQ47
37	183	7.8	769	5	Q24971
38	183	7.8	1299	5	Q28489
39	182	7.7	1622	5	Q06550
40	180.5	7.7	2395	5	Q27167
41	179	7.6	3695	4	Q8TDF8
42	177	7.6	439	5	Q94827
43	176	7.5	419	5	Q8SYE6
44	176	7.5	448	5	Q9W491
45	176	7.5	503	5	Q9U018

ALIGNMENTS

RESULT 1

Q9XZG2 ID Q9XZG2 PRELIMINARY: PRT; 442 AA.

AC Q9XZG2; Q9XZG2; 01-NOV-1999 (Tremblrel. 12, Created)

DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)

DE Immobilization antigen precursor.

GN IAG48.

OS Ichthyophthirius multifiliis.

OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;

OC Ophryoglenina; Ichthyophthirius.

OX NCBI_TaxID=5932;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-G1;

RX MEDLINE=99196987; PubMed=10095108;

RA Clark T.G., Lin T.L., Jackwood D.A., Sherrill J., Lin Y.,

RA Dickerson H.W.;

RT "The gene for an abundant parasite coat protein predicts tandemly

RT repetitive metal binding domains.";

RL Gene 229:91-100(1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-G1;

RA Gaertig J., Gao Y., Tishgarten T., Clark T.G., Dickerson H.W.;

RT "Surface display of a parasite antigen in the ciliate Tetrahymena

RT thermophila.";

RL Nat. Biotechnol. 0:0-0(1999).

DR EMBL: AF140273; AAC31283.1; -.

DR PRINTS: PR01574; TUBBYPROTEIN.

KW Signal.

FT CHAIN 1 20 POTENTIAL.

FT SIGNAL 21 442 IMMOBILIZATION ANTIGEN

SQ SEQUENCE 442 AA; 45025 MW; 52658F3F65D27AFA CRC64;

Query Match 100.0%; Score 2342; DB 5; Length 442;

Best Local Similarity 100.0%; Pred. No. 2.7e-156;

Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SQ		SEQUENCE	395 AA;	39567 MW;	68DA2C790E4FD393	CRC64;
Query Match		89.1%; Score 2087; DB 5; Length 395;				
Best Local Similarity		99.7%; Pred. No. 1.7e-138;				
Matches		389;	Conservative	0;	Mismatches	1; Indels 0; Gaps 0;
QY	20	AVPCPDGTQTQAGLTDVGAADLGTVCNCRPNFYNGGAAQGEANGNQPPFAANNAARGICV	79			
Db	1	AVPCPDGTQTQAGLTDVGAADLGTVCNCRPNFYNGGAAQGEANGNQPPFAANNAARGICV	60			
QY	80	PCQINRVGSVTNAGDLATLATQCTGPTGATDGDGVTDFVDSAAQCKVKCPNFYNGG	139			
Db	61	PCQINRVGSVTNAGDLATLATQCTGPTGATDGDGVTDFVDSAAQCKVKCPNFYNGG	120			
QY	140	SPQGEAPGVQVFAAGAAAAGVAAVTSQVPCQLNKNDSPATAGAANLATQCSNQCPGTG	199			
Db	121	SPQGEAPGVQVFAAGAAAAGVAAVTSQVPCQLNKNDSPATAGAANLATQCSNQCPGTG	180			
QY	200	VLDGVTILVFNSTATLCVKCRPNFYNGGSPQGEAPGVQVFAAGAAAAGVAAVTSQVPC	259			
Db	181	VLDGVTILVFNSTATLCVKCRPNFYNGGSPQGEAPGVQVFAAGAAAAGVAAVTSQVPC	240			
QY	260	QINKNDSPATAGAANLATQCTGPTGATDGDGVTILVFNSTQCSQCIANFYFNGNFE	319			
Db	241	QINKNDSPATAGAANLATQCTGPTGATDGDGVTILVFNSTQCSQCIANFYFNGNLE	300			
QY	320	AGKSQCLKCPVSKTTPAHAPGNATATQATQCLTTCPCAGTVDLDDGSTNMFVASATECTKCSA	379			
Db	301	AGKSQCLKCPVSKTTPAHAPGNATATQATQCLTTCPCAGTVDLDDGSTNMFVASATECTKCSA	360			
QY	380	GFASKTTGTFAGTDTCTECTKLTSGATA	409			
Db	361	GFASKTTGTFAGTDTCTECTKLTSGATA	390			
RESULT 3						
Q962N5		PRELIMINARY; PRT; 460 AA.				
ID	Q962N5;					
AC	Q962N5;					
DT	01-DEC-2001 (Tremblrel. 19, Created)					
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)					
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)					
DE	52kDa Immobilization antigen variant B protein.					
OS	Ichthyophthirius multifiliis.					
OC	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;					
OC	Ophryoglenina; Ichthyophthirius.					
OX	NCBI_TaxID=5932;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=G5;					
RA	Lin Y., Wang J.C., Clark T.C.;					
RT	"Variation in primary sequence and tandem repeat copy number among i-					
RT	antigen genes of Ichthyophthirius multifiliis.";					
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.					
DR	EMBL: AF405431; AAK94941.1; -.					
SQ	SEQUENCE 460 AA; 47535 MW; 55DB1FB3C62F2371	CRC64;				
Query Match		56.9%; Score 1333; DB 5; Length 460;				
Best Local Similarity		54.7%; Pred. No. 1.1e-85;				
Matches		254;	Conservative	58;	Mismatches	126; Indels 26; Gaps 4;
QY	1	MKNLILILILISLFINELRAVPCDGTQTQAGLTDVGAADLGTVCNCRPNFYNGGAAQ	60			
Db	1	MKNLILILILISLFINELRAVPCDGTQTQAGLTDVGAADLGTVCNCRPNFYNGGAAQ	60			
QY	61	EANGNQPPFAANNAARGICVPCQINRVGSVTNAGDLATLATQCTGPTGATDGDGVTDFV	120			
Db	61	EANGNQPPFAANNAARGICVPCQINRVGSVTNAGDLATLATQCTGPTGATDGDGVTDFV	116			
QY	121	DRSAAQCKVKCPNFYNGGSPQGEAPGVQVFAAGAAAAGVAAVTSQVPCQLNKNDSPAT	169			
Db	117	TQSLTQCVNCKPNFYNGGSPQGEAPGVQVFAAGAAAAGVAAVTSQVPCQLNKNDSPAT	176			

SQ		SEQUENCE	395 AA;	39567 MW;	68DA2C790E4FD393	CRC64;
Query Match		89.1%; Score 2087; DB 5; Length 395;				
Best Local Similarity		99.7%; Pred. No. 1.7e-138;				
Matches		389;	Conservative	0;	Mismatches	1; Indels 0; Gaps 0;
QY	20	AVPCPDGTQTQAGLTDVGAADLGTVCNCRPNFYNGGAAQGEANGNQPPFAANNAARGICV	79			
Db	1	AVPCPDGTQTQAGLTDVGAADLGTVCNCRPNFYNGGAAQGEANGNQPPFAANNAARGICV	60			
QY	80	PCQINRVGSVTNAGDLATLATQCTGPTGATDGDGVTDFVDSAAQCKVKCPNFYNGG	139			
Db	61	PCQINRVGSVTNAGDLATLATQCTGPTGATDGDGVTDFVDSAAQCKVKCPNFYNGG	120			
QY	140	SPQGEAPGVQVFAAGAAAAGVAAVTSQVPCQLNKNDSPATAGAANLATQCSNQCPGTG	199			
Db	121	SPQGEAPGVQVFAAGAAAAGVAAVTSQVPCQLNKNDSPATAGAANLATQCSNQCPGTG	180			
QY	200	VLDGVTILVFNSTATLCVKCRPNFYNGGSPQGEAPGVQVFAAGAAAAGVAAVTSQVPC	259			
Db	181	VLDGVTILVFNSTATLCVKCRPNFYNGGSPQGEAPGVQVFAAGAAAAGVAAVTSQVPC	240			
QY	260	QINKNDSPATAGAANLATQCTGPTGATDGDGVTILVFNSTQCSQCIANFYFNGNFE	319			
Db	241	QINKNDSPATAGAANLATQCTGPTGATDGDGVTILVFNSTQCSQCIANFYFNGNLE	300			
QY	320	AGKSQCLKCPVSKTTPAHAPGNATATQATQCLTTCPCAGTVDLDDGSTNMFVASATECTKCSA	379			
Db	301	AGKSQCLKCPVSKTTPAHAPGNATATQATQCLTTCPCAGTVDLDDGSTNMFVASATECTKCSA	360			
QY	380	GFASKTTGTFAGTDTCTECTKLTSGATA	409			
Db	361	GFASKTTGTFAGTDTCTECTKLTSGATA	390			
RESULT 2						
Q27208		PRELIMINARY; PRT; 395 AA.				
ID	Q27208;					
AC	Q27208;					
DT	01-NOV-1996 (Tremblrel. 01, Created)					
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)					
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)					
DE	Immobilization antigen precursor (Fragment).					
OS	Ichthyophthirius multifiliis.					
OC	Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;					
OC	Ophryoglenina; Ichthyophthirius.					
OX	NCBI_TaxID=5932;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=GEORGIA;					
RX	MEDLINE=92335298; PubMed-1631132;					
RA	Clark T.G., McGraw R.A., Dickerson H.W.;					
RT	"Developmental expression of surface antigen genes in the parasitic					
RT	ciliate Ichthyophthirius multifiliis.";					
RL	Proc. Natl. Acad. Sci. U.S.A. 89:6363-6367(1992).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=GEORGIA;					
RX	MEDLINE=93020590; PubMed-1383510;					
RA	Lin T.L., Dickerson H.W.;					
RT	"Purification and partial characterization of immobilization antigens					
RT	from Ichthyophthirius multifiliis.";					
RL	J. Protozool. 39:457-463(1992).					
RN	[3]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=GEORGIA;					
RA	Clark T.;					
RL	Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.					
DR	EMBL: M92907; AAC36158.1; -.					
DR	PRINTS; PR01574; TUBBYPROTEIN.					
KW	Signal.					
FT	NON_TER	1	1	POTENTIAL.		
FT	SIGNAL	<1	1	POTENTIAL.		
FT	CHAIN	2	395	IMMOBILIZATION ANTIGEN.		

RESULT 6	
Q9GPP3	PRELIMINARY; PRT; 316 AA.
AC Q9GPP3	
DT 01-MAR-2001 (TrEMBLrel. 16, Created)	
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)	
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)	
DE Im mobilization antigen LB (Fragment).	
GN SERLB.	
OS Tetrahymena thermophila.	
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;	
OC Tetrahymenina; Tetrahymena.	
OX NCBI_TaxID=5911;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=B;	
RA MEDLINE=20549003; PubMed=11095959;	
RA Doerder F.P., Gerber C.A.;	
RT "Molecular Characterization of the SerL Paralogs of Tetrahymena	
RT thermophila.";	
RL Biochem. Biophys. Res. Commun. 278:621-626(2000).	
DR EMBL; AF312770; AAG38116.1; -.	
FT NON_TER	
SQ SEQUENCE 316 AA; 3008 MW; 133A0B7D0797A3BD CRC64;	
Query Match 9.9%; Score 231; DB 5; Length 316;	
Best Local Similarity 27.7%; Pred. No. 9.1e-09;	
Matches 106; Conservative 24; Mismatches 127; Indels 126; Gaps 21;	
QY 7 LILIIISLFINELRAVPCPDGTQAGLTDVGAADLGTCTVCRPNFYNGGAQGEANGQ 66	
Db 6 LILISLAVIATVNA--CTD-----TNATAGAGGTCTF--CNAGY-----GTSTDVT 47	
QY 67 PFAANNAARGICVPCQINRVGSVTNAGDLATLATQCSQCTGTALDDGVTDVDFRSAQ 126	
Db 48 P-----SGSCTKCTPTGNTSAAATAS--GTLVSSC-----TCNDTNASLKGDNNGCQ 91	
QY 127 CVKCKPNFYNGSGPGEAPGVQVFAAGAAAGVAAVTSQCVPCQLNKNDSPATAGAQA 186	
DR EMBL; AF312771; AAG38117.1; -.	
FT NON_TER	
SQ SEQUENCE 316 AA; 3008 MW; 133A0B7D0797A3BD CRC64;	
Query Match 9.9%; Score 231; DB 5; Length 316;	
Best Local Similarity 27.7%; Pred. No. 9.1e-09;	
Matches 106; Conservative 24; Mismatches 127; Indels 126; Gaps 21;	
QY 7 LILIIISLFINELRAVPCPDGTQAGLTDVGAADLGTCTVCRPNFYNGGAQGEANGQ 66	
Db 6 LILISLAVIATVNA--CTD-----TNATAGAGGTCTF--CNAGY-----GTSTDVT 47	
QY 67 PFAANNAARGICVPCQINRVGSVTNAGDLATLATQCSQCTGTALDDGVTDVDFRSAQ 126	
Db 48 P-----SGSCTKCTPTGNTSAAATAS--GTLVSSC-----TCNDTNASLKGDNNGCQ 91	
QY 127 CVKCKPNFYNGSGPGEAPGVQVFAAGAAAGVAAVTSQCVPCQLNKNDSPATAGAQA 186	
Db 92 ---CKANFY---GTPNAVSGG-----ATGCAQANLATQ 279	
QY 187 LATQCSNQCTGTALDDGVTLVF-----NTSATL-----CVKCRPNFYNGSGPGEAP 235	
Db 107 -ATGCS-ACPTGTTSPAGTAATVSCACNDTNASLKGDNNGC-QCKANFYGTPNAVSGGAT 163	
QY 236 GVQVFAAG-AAAAGVAAVTSQCVPCQINKNDSP-----ATAGAQANLATQ 279	
Db 164 GCTACPTGSAAGAAAGTAVTS---CACNDTNASLKGDNNGCQ 219	
QY 280 CSTQCTGTALDDGVTLVF-----NST-QCSOCIANFYFNGFNFAAGKSCQCLKC 328	
Db 220 C-TACPTGTTSTAGTVIGSCACPDNNAALNSATPVCCOKAN-FYGIPTASGASGCTAC 277	
QY 329 PVSKTTPAHAPGNATQATQCLT 351	
Db 278 PSGOTAPAGSATNVCKAASTST 300	
RESULT 7	
Q9GPP4	PRELIMINARY; PRT; 316 AA.
AC Q9GPP4	
DT 01-MAR-2001 (TrEMBLrel. 16, Created)	
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)	
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)	
DE Im mobilization antigen LA (Fragment).	
GN SERLA.	
OS Tetrahymena thermophila.	
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;	
OC Tetrahymenina; Tetrahymena.	
OX NCBI_TaxID=5911;	
RN [1]	

RESULT 8	
Q9GPP2	PRELIMINARY; PRT; 305 AA.
AC Q9GPP2	
DT 01-MAR-2001 (TrEMBLrel. 16, Created)	
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)	
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)	
DE Im mobilization antigen LC (Fragment).	
GN SERLC.	
OS Tetrahymena thermophila.	
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;	
OC Tetrahymenina; Tetrahymena.	
OX NCBI_TaxID=5911;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=B;	
RA MEDLINE=20549003; PubMed=11095959;	
RA Doerder F.P., Gerber C.A.;	
RT "Molecular Characterization of the SerL Paralogs of Tetrahymena	
RT thermophila.";	
RL Biochem. Biophys. Res. Commun. 278:621-626(2000).	
DR EMBL; AF312772; AAG38118.1; -.	
FT NON_TER	
SQ SEQUENCE 305 AA; 28863 MW; 0568C353A0253564 CRC64;	

12 LAVTQADKCEVTGN-----TEICTQCRARGVPVDFCWPFGFFQAAAGCTEDGGVP--L 65
121 DRSAAQCKVKPNE--YINGGSPQGEA-PGVOVFAAGAAAAGVAAVTSQCVPCLNKN--- 175
66 DKTAATCGKGGDYLFPWGGCYKTESQPSDI--CTAASNGV-----CTECN-TKNGLF 116
176 DSPATAGAQAANLATQCSNQ-----CPTGTVLDDGVTLVFNFTSATILCVKCRPNFY 224
117 KNPATAPKRGRECIILCHDATGADGVMGEGCATCTPTN-----NKGAAATCECQDGY 170
225 YNGSGPQGEAPGVQVFAAGAAAAGVAAVTSQCVPCLN---KNDSPATAGAQAANLATQCS 281
171 NDGGACKKVDGC-IDCTGA-----NOCITCEDGKYLKNQKNOVDAG----- 210
282 TQCPGTATQIDGVTLVFNFSNST-QCSQCIANYFNFNNGFEACKSOLCKPCVSKTTPAHAPG 340
211 -QCDQGT-----YADPTTGCKKPC-----GITCATCEYNATISQPOCK 248
341 NTATQATQCLTTCPCAGTV-LDDGTSTN---FV-----A 369
249 TCSTSNKMWKTRADGTTTCVDGCGCTGNTHFVSGTNQKLCVPCGDTTNGVLGCMTC 308
370 SATETCKKCSAGFASKTTGTTAGTDTCTECTKKLTSGATAKYVABATQKVOCASTTAKF 429
309 SKTCTCKLDGYDYS-----GSGTWTCTAC-----PGANCATLCE-RYKRCQCTCKPGFF 357
430 LSIS 433
358 LKDS 361

RESULT 11
Q9XTJ7 PRELIMINARY; PRT; 709 AA.
ID Q9XTJ7
AC Q9XTJ7
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Variant-specific surface protein (fragment).
GN VSP417-6.
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRIS-136;
RC MEDLINE=99026095; PubMed=9806870;
RA "E. P.L., Darby J.M.;
RT "Giardia intestinalis: conservation of the variant-specific surface
RT protein VSP417-1 (TSA417) and identification of a divergent homologue
RT encoded at a duplicated locus in genetic group II isolates.";
RL Exp. Parasitol. 90:250-261(1998).
DR EMBL: U89266; AAD03483.1; -
DR InterPro: IPR002174; Furin-like.
DR InterPro: IPR005127; Giardia_VSP.
DR InterPro: IPR001239; Kazal_inhib.
DR Pfam: PF03302; VSP; 2.
DR PRINTS: PR00290; KAZALINHBTR.
DR SMART: SM00261; FU; 3
DR NON_TER 709 AA; 71516 MW; 3512BB844B38D134 CRC64;
SQ SEQUENCE 709 AA; 71516 MW; 3512BB844B38D134 CRC64;
Query Match 9.2%; Score 214.5; DB 5; Length 709;
Best Local Similarity 22.9%; Pred. No. 2.9e-07;
Matches 129; Conservative 40; Mismatches 182; Indels 213; Gaps 31;
QY 14 FINEIRA-----VPCPDGTQAGLTDVGAADLGT-----CVNC 47
123 FLNPLRANTKDSVWSCSD-----TAGTDSKTYRGVQYRCRCDGAVLTDAAAGDAKCTRC 178
48 RENFYNGGAAGQEA-----NGNQPFANNAARGI----- 77

179 GENKYLATTTCGEGCTPDTEFSKEDSDNGKRCFACGDDVTTGVASCEKCTPPSPQAKPA 233
78 CVPQCIINRVGSVTNAGDLATLATQCSFQCPGTGTALDDGVTDVDFRASAOCVKCKPNFY 137
239 CTKCGGNNY--LKTADGTTTCAEQSCSPDSPVEN-----SQSGNRCVLC----- 283
138 GGSQGEAPGVQVFAAGAAA--AGVAAVTSQCVPCLN---QLNKNDSPATAGAQAANLATQ 190
284 GDAANG---GVDKCAACTPADKGRAAPAVTCTACTDGYKPSADKTTTCEAVSSCKTPGCKA 340
191 CSNQCPTGTVLDD--DGVTLVFNFTSATL----- 215
341 CSNEKENEVCTDCDGTSTYLPSTQCSIDCAKYNVYGAIEGAKKLCKECTRANCKTCDG 400
216 ---CVKCRPNFYNGG--SPOGEAPGVQVFAAGAAAAGVAAVTSQCVPCLN--- 263
401 QGRQCTCSGDFYKNGDACSPCHE-----SKTCSAGTA---SDCTEPTGKALRYGDD 450
264 -----NDSPATAGAQAANLATQCSFQCPGTGTAL--QDGV-----TLVFS 299
451 GTKGTCGAGCATGGSGACKTCGLTIDGASYCS--ECATATEYEPQNGVCAKPSARATPTCN 509
300 NBSSTQ---CSQCIANYF-FNGN-FEA---GKSQCLKPCVSKTTPAHAPONTATQATQCL 350
510 DSPIQNGVCGTCAANSYFKMNGGCVETVKYPGKTVICISAPNGGTCKAAADGYKLDSTG--L 567
351 TTCPCAG-----TVLDDGTSTNFSVATSECTCSAGFTASKT-----T 387
568 TVCSGCKECTSSDCTTCLD-----GYVKSASACTKCD---FSCETCNGAATTCACAT 619
388 GF---TAGTDTCTECTKKLTSGAT 408
620 GYKKTASGAGACTSCESD-SNGVT 642

RESULT 12
Q9U048 PRELIMINARY; PRT; 704 AA.
ID Q9U048
AC Q9U048;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Variant-specific surface protein.
GN VSP417-6.
OS Giardia lamblia (Giardia intestinalis).
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=5741;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-AD-1;
RA "E. P.L., Darby J.M.;
RT "A new member of the vsp417 subfamily of variant-specific surface
RT protein (VSP) genes in Giardia intestinalis.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF065606; AAF02907.1; -
DR InterPro: IPR002174; Furin-like.
DR InterPro: IPR005127; Giardia_VSP.
DR Pfam: PF03302; VSP; 2.
DR SMART: SM00261; FU; 4.
DR SEQUENCE 704 AA; 71677 MW; 7E5AE1245AD4FD45 CRC64;
Query Match 9.1%; Score 212.5; DB 5; Length 704;
Best Local Similarity 23.3%; Pred. No. 4e-07;
Matches 129; Conservative 42; Mismatches 190; Indels 193; Gaps 17;
QY 14 FINEIRA-----VPCPDGT-----QTAG-----LTDVGAADLGTVCNCRPN 50
121 FLNPLRANTKDSVWSCSDTTGFTDSKTYRGVQYRCRCDGAAALTDAAAGD-AKCTRCGD 17
51 FYNNGGAAGQEA-----NGNQPFANNAARGI---CVPQCIINRVGSVTNAGDL 95
180 KYLATTTCGEGCTPDTEFSKEDSDNGKRCFACGDDVTTGVASCEKCT-----TPSPDQA 23

Db 162 TRPSQISENTGKEATCTECNANLYLKAVSSPTSATSVCSAEDCKTG-----YFPT 212
QY 212 SATL-----CVKCRPNFYNGSGPOGAPGVQVFAAGAAAGAAVAVTSOCVPCQINKNDS 266
Db 213 TDTTDSKKKCLAT-----STADKGGIDGCSACELLPTTTRASTVLISCSACSTN-NLS 264
QY 267 PATAGAAANLATQCSQCPTGTAIQDGVTLVFSNDSSTQCSQCIANYFFNGFNAEAGKSACL 326
Db 265 P-----LNKNCMODCPAGTYADSNVC---KPCHTSCACKGD-----NTE---SSCT 305
QY 327 KCPVSKTTPAHAPGNATQATQ-----CLTTCPCAGTVLD---DGTSTNFVASATECTKCS 378
Db 306 AC-----YPGSVLSVGTDTNFKTCIAEC-TCKYLENCADGGCTATAGSKVCSCK 355
QY 379 AGFF-----ASKTTGFTAGTDTCTCEYKK--LTSGA----- 407
Db 356 SGFVPPVNGLCVSAETARAAPPSTPDKNG-----VCTACTERYFLESGGCVQAEKFP 409
QY 408 -TAKVVAEATOKVOCAS 423
Db 410 NTLCTTADAGKCTTCAN 426

RESULT 15

Q07317 PRELIMINARY; PRT; 597 AA.
AC Q07317; 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Variant-specific surface antigen 1267 precursor (VSP1267).
GN VSP1267.
OS Giardia intestinalis.
OC Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
OX NCBI_TaxID=5741;
[1]
SEQUENCE FROM N.A.
RP STRAIN=ATCC 30957 / WB;
RC MEDLINE=92131058; PubMed=1775165;
RX Mowatt M.R., Aggarwal A., Nash T.E.;
RA "Carboxy-terminal sequence conservation among variant-specific surface
RT proteins of Giardia lamblia.";
RL Mol. Biochem. Parasitol. 49:215-228(1991).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
DR EMBL: M63966; AAA29159.1;
DR InterPro: IPR000564; 2Fe2S-ferredoxin.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002174; Furin-like.
DR InterPro: IPR005127; Giardia_VSP.
DR Pfam: PF03302; VSP; 1.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00261; FU; 5.
DR PROSITE: PS00197; 2FE2S-FERREDOXIN; 1.
KW Multigene family; Repeat; Signal; Transmembrane; Glycoprotein;
KW Antigen.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 597 VARIANT-SPECIFIC SURFACE PROTEIN 1267.
FT DOMAIN 18 563 EXTRACELLULAR (BY SIMILARITY).
FT DOMAIN 38 528 23 x 4 AA REPEATS OF C-X-X-C.
FT TRANSMEM 564 591 POTENTIAL.
FT DOMAIN 592 596 CYTOPLASMIC (BY SIMILARITY).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 559 559 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 597 AA; 60646 MW; E107846B8BF72202 CRC64;

Query Match 9.0%; Score 210.5; DB 5; Length 597;
Best Local Similarity 22.6%; Pred. No. 4.7e-07;
Matches 125; Conservative 50; Mismatches 188; Indels 189; Gaps 33;

QY 5 ILLILLISLFINELRAVPCPD-GTQOAGLTD-VGAADL-----GTC----- 44
Db 4 IAFYLIILSTF-----AVDCRNSGSCAGQCDDTIGDTEICMQCNQGVKVPINGICTAHSEE 58

QY 45 -----VNCRPN-----FYNGGAAQ-GEANGN-----QPFAANNAAR-- 75
Db 59 AVTNAGCKKNGGTNIEBDRKVCQGCGNGYFLHKGCCYKIGEAPGNLICADEASNPGARTA 118
QY 76 GICVPCQINRVSGVSTNAGDLATATQC-----STOCPT-GTALDDGVTDVFD-----RS 123
Db 119 GVCGAC---KDYKYKNSDAVAT-ADSCIACEDANCATCGGAGENKCTKIDGVFVGATGN 174
QY 124 AAQCVKCK---PNFYNGG-----SPOGEAPGVQVFAAGAAAAGVAAVTSOCVCP--C 170
Db 175 EGGCIKCDATTGPNYSYKGVAGCAKCEKPKNAGPAKCIETCAADYLTKEADEQTSCVSEAVC 234
QY 171 QLNKNDSPAT--AGAQAANLATQCSNQCPGTGVLDGV-----TLVFNTSAT-----LCVK 218
Db 235 REGKTHPTTDSAGNKKVCVSC-----GTTNNGGIENGCECTSKESAARAGTEITCTK 288
QY 219 CRPNFYNGSGPOGEA-----PGVQVFAAGAAAAGVAAVTSOCVPCQINKNDSPTA-- 270
Db 289 CSS-----NNLSPLGDACLITDCPAGTYAVSGDSGSVCKPCHNTCAGCQTDDRETSCACYP 344
QY 271 -----GAQANLATQCS-----TOCPTGTAIQDGV----- 294
Db 345 GYLLYESNGATGRCKEECTGAFITNCADGGCTANVGSAKYCTOCKDGYAPIDGICTAVA 404
QY 295 -----TLVFSNSTQCSQCIANY-----FFNGNFEAGKSQCL-----KCPVSKT-T 334
Db 405 AAGRDVSVCTATGGKCTACTGNYALLSGGCYNTQTLPKSVCKAVANSNDGKC---KTCA 461
QY 335 PAHAPGNATQATQCLTCTCPAGTVLDGDTSTNFVASATECTKCSAGFASKTTGTAGTD 394
Db 462 NGQAPDPATNFCPLGCDSTCAECSTKND-----ADACTKCPFGYY---KTG-----N 504
QY 395 TCTECTCKKLTS 406
Db 505 KCIRCTESSNNG 516

Search completed: February 11, 2003, 19:47:52

Job time : 32.6571 secs